

Qy	564 LPD 566	Query Match	99.4%	Score 1754;	DB 2;	Length 568;
RESULT	2	PRELIMINARY;	PRT;	567 AA.		
ID	Q62380	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	TNF RECEPTOR-ASSOCIATED FACTOR 3 (TRAFAMN).					
GN	TRAF3 OR TRAFM.					
OS	MUS MUSCULUS (MOUSE).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RC	EUTHERIA; RODENTIA.					
RN	[1] SEQUENCE FROM N.A.					
RP	STRAIN=C57BL/6GJ; TISSUE=Brain;					
RC	WANG X., BORNHAAGER B., HAUB O., TOMIHARA - NEWBERGER C.,					
RA	RONBERG N., DINULOS M.B., DISTECHE C.M., COPELAND N.,					
RA	GILBERT D. J., JENKINS N. A., LACY E.;					
RA	SUBMITTED (AUG-1996) TO EMBL/GENBANK/DBJ/ DATA BANKS.					
DR	EMBL: U33840; G1488198; -.					
DR	MGD: MGI:108041; TRAF3;					
SQ	SEQUENCE 567 AA; 64376 MW; 7F4F873B CRC32;					
RESULT	2	PRELIMINARY;	PRT;	567 AA.		
ID	Q62380	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	MEDLINE; 95184010.					
RX	CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.;					
RL	SCIENCE 267:1494-1498 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U21092; G72608;					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64460 MW; 7748CBDB CRC32;					
RESULT	3	PRELIMINARY;	PRT;	568 AA.		
ID	Q13076	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	LMP1 ASSOCIATED PROTEIN.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	MEDLINE; 95184010.					
RX	CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.;					
RL	SCIENCE 267:1494-1498 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U21092; G72608;					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	MEDLINE; 95184010.					
RX	CHENG G., CLEARY A.M., YE Z.S., HONG D.I., LEDERMAN S., BALTIMORE D.;					
RL	SCIENCE 267:1494-1498 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U21092; G72608;					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MEDLINE; 95163092.					
RA	MOSTALOS G., BIRKENBACH M., YALAMANCHILLI R., VANARSDALE T., WARE C.,					
RA	KIEFF E.;					
RA	CELL 80:389-399 (1995).					
CC	-1- SIMILARITY: CONTAINS A C3HC4 -CLASS ZINC FINGER.					
DR	EMBL: U19260; G675460; -.					
DR	PROSITE: PS00518; ZINC_FINGER_C3HC4; 1.					
KW	ZINC-FINGER.					
SQ	SEQUENCE 568 AA; 64490 MW; 073D0015 CRC32;					
RESULT	4	PRELIMINARY;	PRT;	568 AA.		
ID	Q13114	Best Local Similarity 99.2%	Pred. No. 0.00e+00;			
AC	AC_01-NOV-1996 (TREMBLREL. 01, CREATED)	Matches 241;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)					
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)					
DE	CD40 RECEPTOR ASSOCIATED FACTOR 1.					
GN	CRAF1.					
OS	HOMO SAPIENS (HUMAN).					
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;					
RN	[1] SEQUENCE FROM N.A.					
RP	TISSUE-LYMPHOID TUMOR;					
RX	MED					

DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)	Db	348	AVLEEPTNKHDTHINHKAOLSKNEERFKLEGTCTYNGKLWVTDYKMKKRAVDGHTV 407
DT	01-JAN-1998	(TREMBLREL. 05, LAST ANNOTATION UPDATE)	QY	378	GLLESOLSRDQTLSEVHDPLAADDLRFQVLETSYNGLWVTDYKMKKRAVDGHTV 437
DE		TRAF5, MUS MUSCULUS (MOUSE).	Db	408	SIFSOFSYTSRCGTYRLCARAYLNGDGSGRSHSLFVYMRGEFDLSLQWPFFQRVTML 467
OS		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	QY	438	SISQSFYTGFGYKMCARYLNGDGMGTHSLFFVYMRGEYDALLWPWPFQKVTLML 497
OC		EUTHERIA; RODENTIA.	DB	468	LDQ-SEGKKNIMETEKPDPNSSKFKRPDGMMNIAAGCPVPTVHSLVLENKAVNAYTKDDTLFL 526
RN		SEQUENCE FROM N.A.	QY	498	MDQGSSRRHIGDAFKPDPNSSFKRPDGMMNIAAGCPVPTVLENG-TYIKDDTIFI 555
RP		STRAIN-BALB/C.	DB	527	KVAVDLDLDED 537
RC		MEDLINE: 96278943.	QY	556	KVIVNTSDLPD 566
RX		NAKANO H., OSHIMA H., CHUNG W., WILLIAMS-ABBOTT L., WARE C.F.,	RESULT	10	PRELIMINARY;
RA		YAGITA H., OKUNURA K.,	ID	Q13077	PRT;
RA		J. BIOL. CHEM. 271:14661-14664(1996).	AC	Q13077;	416 AA.
RL		CC - SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	DT	01-NOV-1996	(TREMBLREL. 01, CREATED)
CC		MGD: MGI:107548; TRAF5.	DT	01-NOV-1996	(TREMBLREL. 01, LAST SEQUENCE UPDATE)
DR		PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.	DT	01-NOV-1996	(TREMBLREL. 01, LAST ANNOTATION UPDATE)
KW		ZINC_FINGER.	DE	DE	EPSTEIN-BARR VIRUS-INDUCED PROTEIN.
SQ	SEQUENCE	558 AA; 64154 MW; 910ACC60 CRC32;	OS	OS	HOMO SAPIENS (HUMAN).
QY		Score 908; DB 10; Length 558;	OC	OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
DB	324	Score 908; DB 10; Length 558;	RA	RA	EUTHERIA; PRIMATES.
QY		Best Local Similarity 50.4%; Pred. No. 1.15e-152;	RA	RA	SEQUENCE FROM N.A.
DB	372	Best Local Similarity 50.4%; Pred. No. 1.15e-152;	RC	RC	TISSUE-PLEMPHOID TUMOR;
QY		Matches 124; Conservative 58; Mismatches 59; Indels 5; Gaps 4;	RA	RA	MOSIALOS G., BIRKENBACH M., YALAMANCHILI R., VANARSDALE T., WARE C.,
DB	314	Score 908; DB 10; Length 558;	RL	RL	SUBMITTED (MAR-1995) TO EMBL/GENBANK/DBJ/ DATA BANKS.
QY		3HTDKSAWLRQVRHLLQI-VNOQPSRLDLRSYDAVDSVKORTITOLEASDQRV-LLEG 371	DR	DR	EMBL; U19261; G675462; -
DB	324	Score 908; DB 10; Length 558;	SEQUENCE	416 AA;	Score 730; DB 2; Length 416;
QY		3QAEKILKEKEIRERFRQWEEADSMKSSYESLNRVTEL-ESTDKSGQAARTGLIES 382	QY	46163 MW;	Best Local Similarity 51.3%; Pred. No. 1.0e-116;
DB	372	Score 908; DB 10; Length 558;	DB	760442EC CRC32;	Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
QY		ETSKHDAHINHKAOLNKNKEERFKLEGACYSGGLWVTDYKWKREAVEGHTVSFSQ 431	QY		Query Match 41.48;
DB	383	Score 908; DB 10; Length 558;	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
QY		QLSRHDQTSYHDILRLADMLRFQVLETSYNGLWVTDYKWKREAVEGHTVSFSQ 442	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
DB	432	Score 908; DB 10; Length 558;	DB		Query Match 41.48;
QY		PEYTSICGTYRCARAYLNGDGSGRGTHLSYFVYMRGEFDLSLQWPFFQRVTMLLDSG 491	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
DB	443	Score 908; DB 10; Length 558;	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
QY		PFYTGFYFGYKMCARYLNGDGMGTHSLFFVYMRGEYDALLWPFFQKVTLMLDQG 502	DB		Query Match 41.48;
DB	492	Score 908; DB 10; Length 558;	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
QY		KRNHIVETKADPNSSSFVADPSVSHLSTENKNTYIKDDT1FLKYAVD 551	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
DB	503	Score 908; DB 10; Length 558;	DB		Query Match 41.48;
QY		SRRHLDGDAFKPDPNSSFKRPGENNIAAGCPVSHLSTENKNTYIKDDT1FLKYAVD 560	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
DB	552	Score 908; DB 10; Length 558;	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
QY		LTDED 557	DB		Query Match 41.48;
DB	561	Score 908; DB 10; Length 558;	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
QY		TSQSLPD 566	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
RESULT	9	PRELIMINARY;	DB		Query Match 41.48;
ID	000463	PRELIMINARY;	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
AC	000463;	PRT;	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
DT	00-04-63;	CREATED)	DB		Query Match 41.48;
DT	01-JUL-1997	(TREMBLREL. 04, CREATED)	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
DT	01-JUL-1997	(TREMBLREL. 04, LAST SEQUENCE UPDATE)	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
CC		GENOMICS:42:26-32(1997).	DB		Query Match 41.48;
CC		-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
DR		EMBL; U69108; G2138180; -.	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
DR		PROSITE; PS00518;	DB		Query Match 41.48;
KW		ZINC_FINGER.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
OS		HOMO SAPIENS (HUMAN).	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
OC		EUOKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	DB		Query Match 41.48;
OC		EUTHERIA; PRIMATES.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
RN		SEQUENCE FROM N.A.	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
RX		MEDLINE; 97321041.	DB		Query Match 41.48;
RA		NAKANO H., SHINDO M., YAMADA K., YOSHIDA M.C., SANTEE S.M., WARE C.F.,	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
RA		JENKINS N.A., GILBERT D.J., YAGITA H., COPELAND N.G., OKUMURA K.,	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
RA		GENOMICS:42:26-32(1997).	DB		Query Match 41.48;
RA		-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
RA		EMBL; U69108; G2138180; -.	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
RA		PROSITE; PS00518;	DB		Query Match 41.48;
KW		ZINC_FINGER.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
OS		HOMO SAPIENS (HUMAN).	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
OC		EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	DB		Query Match 41.48;
OC		EUTHERIA; PRIMATES.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
RN		SEQUENCE FROM N.A.	DB		Query Match 41.48;
RX		MEDLINE; 95166958.	DB		Best Local Similarity 51.3%; Pred. No. 1.0e-116;
RA		SONG H.Y., DONNER D.B.;	DB		Matches 100; Conservative 50; Mismatches 41; Indels 4; Gaps 3;
RA		BIOCHEM. J. 309:825-829(1995).	DB		Query Match 41.48;

RN	[2]	SEQUENCE FROM N.A.
RP		SEQUENCE FROM N.A.
RX		SEQUENCE FROM N.A.
RA	94343371.	
RA	ROTHIE M., WONG S.C., HENZEL W.J., GOEDDEL D.V.,	
RL	CELL 78:681-692 (1994).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RA	SONG H.Y.,	
RL	SUBMITTED (JUL-1994) TO EMBL/GENBANK/DDBJ DATA BANKS.	
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	
DR	EMBL; U12597; G915273; -;	
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 2.	
KW	ZINC-FINGER.	
SQ	SEQUENCE 501 AA; 55794 MW; 1C62BC1F CRC32;	
Query Match	37 6%; Score 663; DB 2; Length 501;	
Best Local Similarity	47.3%; Pred. 5.22e-103;	
Matches	88; Conservative 49; Mismatches 47; Indels 2; Gaps 2;	
Db	317 LSSKQQLERSIGLKLAMADLEQKTYRPFQOCGHRYCSCCLASLIRKQEAVGRIPAI 376	
Qy	380 LESQLSRHDQTSVHDTRLADMFLRQVLE-TASYNGVLKIRKRRQEAVGKTLSL 439	
Db	377 FSPAFITSRGKMKCIRIYNGDGTGRGTHLSSLFFVYVMIGPNDALLPNPQNYTMLD 436	
Qy	440 YSQPFITGYFGYKMKCIRVYANGDGMGKTFHLSLEFPVIRGSEYDALLPFPKQKVTLMLD 499	
Db	437 Q-NRREHVIDAFRPDYTSFSSFORPYNDMNTIASGGPFLCPVSKMBAKNSVYRDAIFIKAI 495	
Qy	500 QGSSRHLGDAFKPDENSSFFKKPKPGEYNTASGGPVEYQTVI-NSYKDDTIFKVI 558	
Db	496 VDLTGL 501	
Qy	559 VDTSDL 564	
RESULT	12	PRELIMINARY; PRT; 470 AA.
ID	Q14848	SEQUENCE FROM N.A.
AC	Q14848;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	CYSSTEIN RICH DOMAIN ASSOCIATED TO RING AND TRAF PROTEIN.	
GN	MLN 62, CARTI.	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;	
RX	MEDLINE: 96039245	
RA	TOMASETTI C., REGNIER C.H., MOOG-LUTZ C., MATEEI M.G., CHENARD M.P.,	
RA	LIDEREAU R., BASSET P., RIO M.C., GENOMICS 28:367-376 (1995).	
RL	[2]	
RN	RP	SEQUENCE FROM N.A.
RC	TISSUE=BREAST DERIVED METASTATIC LYMPH NODE;	
RX	MEDLINE: 96029665.	
RA	REGNIER C.H., TOMASETTI C., MOOG-LUTZ C., CHENARD M.P., WENDLING C., BASSET P., RIO M.C.; J. BIOL. CHEM. 270:25715-25721 (1995).	
RA	ZINC-FINGER.	
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	
DR	EMBL; X80200; G911277; -;	
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.	
KW	ZINC-FINGER.	
SQ	SEQUENCE 470 AA; 53443 MW; F3B78A90 CRC32;	
Query Match	24.8%; Score 437; DB 2; Length 470;	
Best Local Similarity	40.0%; Pred. No. 5.51e-59;	
Matches	68; Conservative 44; Mismatches 44; Indels 11; Gaps 7;	
Db	294 EIRRELEELSYSGDGLWIKIGSGRRLQEAKAPNLECSFPAFYTHYGYKLVQVSFLN 353	
Qy	517 SSSFKKP-T-GEMN1AS--GCPVFVATQVLENGTYIKDDTIFKIVD 560	
RESULT	13	PRELIMINARY; PRT; 470 AA.
ID	Q51382	SEQUENCE FROM N.A.
AC	Q51382;	
DT	01-NOV-1996 (TREMBLREL. 01, CREATED)	
DT	01-NOV-1996 (TREMBLREL. 01, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	CYSSTEINE RICH MOTIF ASSOCIATED TO RING AND TRAF DOMAINS PROTEIN CARTI.	
GN	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	REGNIER C.H.;	
RA	SUBMITTED (OCT-1995) TO EMBL/GENBANK/DDBJ DATA BANKS.	
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	
DR	EMBL; X92346; G104446; -;	
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.	
KW	ZINC-FINGER.	
SQ	SEQUENCE 470 AA; 53418 MW; 4296B389 CRC32;	
Query Match	23 1%; Score 407; DB 10; Length 470;	
Best Local Similarity	38.8%; Pred. No. 3.0e-53;	
Matches	66; Conservative 45; Mismatches 48; Indels 11; Gaps 7;	
Db	294 EIRRELEELSYSGDGLWIKIGSGRRLQEAKAPNLECSFPAFYTHYGYKLVQVSFLN 353	
Qy	402 DLREFQVLE-TASYNGVLKIRKRRQEAVGKTLSL 439	
Db	354 GNGSGEGPHLSIYRVLGAFNDLLEPLAREYFSLDQDGPGLAKPQHVTETFHDPN 413	
Qy	461 GDNMGKGSGLSLEFPVIRGEGYDALLPFPKQKVTLMLDQG--S-SR-RHLGDAFKPDPN 516	
Db	414 WKFQKPEWTWGRSLDESSLGFGYPKFTSHQDTRKRNVRDADVIFRASVE 463	
Qy	517 SSSFKKP-T-GEMN1AS--GCPVFVATQVLENGTYIKDDTIFKIVD 560	
RESULT	14	PRELIMINARY; PRT; 530 AA.
ID	P70196	SEQUENCE FROM N.A.
AC	P70196;	
DT	01-FEB-1997 (TREMBLREL. 02, CREATED)	
DT	01-FEB-1997 (TREMBLREL. 02, LAST SEQUENCE UPDATE)	
DT	01-JAN-1998 (TREMBLREL. 05, LAST ANNOTATION UPDATE)	
DE	TNF RECEPTOR-ASSOCIATED FACTOR 6 (TRAF6).	
GN	MUS MUSCULUS (MOUSE).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; RODENTIA.	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RA	ISHIDA T., MIZUSHIMA S., AZUMA S., KOBAYASHI N., TOJO T., SUZUKI K., AIZAWA S., WATANABE T., MOSTAHL G., KIEFF E., YAMAMOTO T., INOUÉ J.;	
CC	-1- SIMILARITY: CONTAINS A C3HC4-CLASS ZINC FINGER.	
DR	EMBL; D84655; G1651195; -;	
DR	MGI: MGI:108072; TRAF6.	
DR	PROSITE; PS00518; ZINC_FINGER_C3HC4; 1.	
KW	ZINC-FINGER.	
SQ	SEQUENCE 530 AA; 60082 MW; C500CCCTTCCCTCCCT 353	

Query	Match	6.6%	Score 117; DB 3; Length 284;
	Best Local Matches	17.3%; Conservative	Pred. No. 7.04e-03; Mismatches 26; Indels 35; Gaps 1;
	13;		
Db	41	EEVRALORKIQDQENEDQVOEQLSANTKLEEKALQTAEGDYAALNRQIOLIEDE 100	
Db	327	EKIKELEDEIRPFRQWEEA-DSMRKSSVESLQRVTEYDVKSGAQARNTGILLESOL 385	
Db	101	RSEERLKATAKLE 115	
Db	386	RHDPTSYHDTRAD 400	
Or			

Search completed: Thu Aug 6 14:09:57 1998
Search time: 89 secs.